



Sheet For, PTO-1449

INFORMATION DISCLOSURE
IN AN APPLICATION

(Use several sheets if necessary)

Docket Number
109845.193US1Application Number
- 10/057,789Applicant
Haynes et al.

Filing Date

January 25, 2002

Group A

1648

Sheet 1 OF 1

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U.S. Patent Documents

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE

Foreign Patent Documents

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION
						YES NO
JR	WO 97/35887	Oct 2, 1997	PCT			
JR	WO 00/11208	Mar 2, 2000	PCT			
JR	WO 01/96539	Dec 20, 2001	PCT			

Other Documents (Including Author, Title, Date Pertinent Pages, Etc.)

JR A1	Cai et al., "Recombinant Phycobiliproteins", Analytical Biochemistry, 2001, Vol. 290(2), pp 166-204
JR A2	Gygi et al., "Quantitative Analysis of Complex Protein Mixtures Using Isotope-Coded Affinity Tags", Nature Biotechnology, Oct. 1999, Vol. 17, No. 10, pp 994-999
JR A3	Higashiura et al., "The Chemical Conversion of Carboxyl-Terminal Glycines in Peptides into Taurine", Journal of the Chemical Society Chemical Communications" No. 9, 1989, pp 521-522
JR A4	Kapust and Waugh, "Controlled Intracellular Processing of Fusion Proteins by TEV Protease", 2000, Vol. 19(2), pp 312-318
JR A5	Virgiello et al., "Organic Preparations and Procedures International, 1972, pp 43-47, Vol. 4, No. 1

EXAMINER

Jeffrey E. Russell

DATE CONSIDERED

April 28, 2004

EXAMINER: Initial if citation is considered, whether or not citation is in conformance with MPEP § 609: Draw Line through citation if not conformance and not considered. Include copy with next communication to applicant.

FORM PTO-1449	U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTY. DOCKET NO. NADII 022A	APPLICATION NO. 10067,789
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (USE SEVERAL SHEETS IF NECESSARY)		APPLICANT Haynes et al.	RECEIVED OCT 08 2002 TECH CENTER 1600/2900
		FILING DATE January 25, 2002	



U.S. PATENT DOCUMENTS						
EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE (IF APPROPRIATE)
1	5,538,897	07/23/96	Yates			

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)					
JR	2	Boucherie et al., Two-dimensional gel protein database of <i>Saccharomyces cerevisiae</i> , <i>Electrophoresis</i> 17:1683-1699 (1996)				
JR	3	Dong'e et al., Emerging tandem-mass-spectrometry techniques for the rapid identification of proteins, <i>Trends Biotechnol</i> 15:418-425 (1997)				
JR	4	Ducret et al., High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry, <i>Prot Sci</i> 7:706-719 (1998)				
JR	5	Eng et al., An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database, <i>J Am Soc Mass Spectrom</i> 5:976-980 (1994)				
JR	6	Figgeys and Aebersold, High sensitivity analysis of proteins and peptides by capillary electrophoresis-tandem mass spectrometry: Recent developments in technology and applications, <i>Electrophoresis</i> 19:885-892 (1998)				
JR	7	Figgeys et al., A microfabricated device for rapid protein identification by microelectrospray ion trap mass spectrometry, <i>Anal Chem</i> 69:3153-3160 (1997)				
JR	8	Figgeys et al., Protein identification by solid phase microextraction—capillary zone electrophoresis—microelectrospray—tandem mass spectrometry, <i>Nature Biotech</i> 14:1579-1583 (1996)				
JR	9	Garrels et al., Proteome studies of <i>Saccharomyces cerevisiae</i> : Identification and characterization of abundant proteins, <i>Electrophoresis</i> 18:1347-1360 (1997)				
JR	10	Gygi et al., Quantitative analysis of complex protein mixtures using isotope-coded affinity tags, <i>Nature Biotechnol</i> 17:994-999 (1999)				
JR	11	Gygi et al., Correlation between protein and mRNA abundance in yeast, <i>Cell Biol</i> 19:1720-1730 (1999)				
JR	12	Gygi et al., Protein analysis by mass spectrometry and sequence database searching: Tools for cancer research in the post-genomic era, <i>Electrophoresis</i> 20:310-319 (1999)				
JR	13	Haynes et al., Identification of gel-separated proteins by liquid chromatography-electrospray tandem mass spectrometry: Comparison of methods and their limitations, <i>Electrophoresis</i> 19:939-945 (1998)				
JR	14	Link et al., Identifying the major proteome components of <i>Haemophilus influenzae</i> type-strain NCTC 8143, <i>Electrophoresis</i> 18:1314-1334 (1997)				
JR	15	Link et al., Direct analysis of protein complexes using mass spectrometry, <i>Nat Biotech</i> , 17:676-682 (1999)				
JR	16	Mann and Wilm, Error-tolerant identification of peptides in sequence databases by peptide sequence tags, <i>Anal Chem</i> 66:4390-4399 (1994)				

EXAMINER	Jeffrey G. Russell	DATE CONSIDERED	April 28, 2004
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FORM PTO-1449	U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTY. DOCKET NO. NADL022A	APPLICATION NO 10057.789
INFORMATION DISCLOSURE STATEMENT BY APPLICANT		<div style="text-align: right;">RECEIVED</div> <div style="text-align: right;">OCT 08 2002</div>	
USE SEVERAL SHEETS IF NECESSARY)		APPLICANT Haynes et al.	<div style="text-align: right;">TECH CENTER 1600/2900</div>
		FILING DATE January 25, 2002	

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)
<i>JR</i>	17 Opitek <i>et al.</i> , Comprehensive on-line LC/LC/MS of proteins, <i>Anal Chem</i> 69:1518-1524 (1997)
<i>JR</i>	18 Pennington <i>et al.</i> , Proteome analysis: from protein characterization to biological function, <i>Trends Cell Bio</i> 7:168-173 (1997)
<i>JR</i>	19 Shalon <i>et al.</i> , A DNA microarray system for analyzing complex DNA samples using two-color fluorescent probe hybridization, <i>Genome Res</i> 6:639-645 (1996)
<i>JR</i>	20 Shevchenko <i>et al.</i> , Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels, <i>Anal Chem</i> 68:850-858 (1996)
<i>JR</i>	21 Shevchenko <i>et al.</i> , Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gels, <i>Proc Natl Acad Sci USA</i> 93:14440-14445 (1996)
<i>JR</i>	22 Velculescu <i>et al.</i> , Characterization of the Yeast Transcriptome, <i>Cell</i> 88:243-251 (1997)
<i>JR</i>	23 Yates <i>et al.</i> , Method to correlate tandem mass spectra of modified peptides to amino acid sequences in the protein database, <i>Anal Chem</i> 67:1426-1436 (1995)

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